REMARKS

Claims 5-10, 12, 14-17 and 19-45 have been cancelled. New claims 58-94 are submitted herein. Applicants respectfully request consideration and allowance of claims 58-94 in view of the following remarks.

Applicants have amended the paragraph beginning at page 11, line 31, to add identifiers for the sequences listed in Figure 3. Applicants also submit herewith a corrected Sequence Listing, which includes all the sequences in Figure 3.

Applicants have amended the paragraph beginning at page 30, line 22, to indicate that coding regions for the dwf4 gene in Figure 10 are designated by an open bar. This amendment serves to correspond the specification with the figure.

Support for the amendments and new claims 58-94 is found throughout the specification. See, e.g., page 18, lines 6-21, and page 69, line 23 to page 70, line 5.

Objections

The Examiner objected to Figure 3 for failing to include sequence identifiers for sequences other than SEQ ID NO:2. Corrected Figure 3, submitted herewith, contains sequence identifiers for all remaining sequences in the figure. The Examiner is requested to withdraw the objection to Figure 3.

The Examiner objected to Figure 10 because of a discrepancy between the specification and the figure in the designation of the coding regions. Applicants have amended the specification at page 30, line 25, to remove the discrepancy. The Examiner is requested to withdraw the objection to Figure 10.

Applicants have also included corrected informal drawings for Figures 1, 3, 9, 10 and 12, for the convenience of the Examiner.

Rejection under 35 USC 112, 2^{d} paragraph.

The Examiner rejected claims 7, 12, 14-17, 19 and 43-45 as being indefinite with respect to claim dependency and the recitation of modulating a dwf4 polypeptide. Without acquiescing

in the rejection, Applicants have cancelled these claims, thereby mooting the rejection. New claims 58-94 are believed to have proper claim dependency, and do not recite modulating a dwf4 polypeptide. The Examiner is requested to withdraw the rejection under 35 USC 112, 2^{d} paragraph.

Rejection under 35 USC 112, 1st paragraph.

The Examiner rejected claims 5-6, 8-10, 12, 14-17, 19 and 20-45 for lack of written description and enablement. Without acquiescing in the rejection, Applicants have cancelled these claims, thereby mooting the rejection. New claims 58-94 do not recite polynucleotides having 15 or 30 contiguous nucleotides, reverse complement, or alteration of phenotypes. New claims 58-94 are believed to have proper written description in, and be enabled by, the specification. The Examiner is requested to withdraw the rejection under 35 USC 112, 2^{d} paragraph.

Conclusion

Attached is a marked-up version of the changes being made by the current amendment.

Applicant respectfully requests reconsideration and allowance of claims 58-94. Enclosed is a $543.00 check for payment of the $375.00 fee for the Request for Continued Examination and $168.00 for four (4) excess independent claims fee; and a $465.00 check for the Petition for a Three-Month Extension of Time fee. Please apply any deficiencies or credits to Deposit Account No. 06-1050.

Respectfully submitted,

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Version with markings to show changes made

In the specification:

Paragraph beginning at page 11, line 31, to page 12, line 13 has been amended as follows:

Figure 3 depicts alignment of cytochrome P450 proteins that exhibited the most similarity to DWF 4 (SEQ ~~Seq~~ ID NO[.]:2) in BLAST searches. GenBank accession numbers are AF044216 (DWF4; CYP90B) (SEQ ~~Seq~~ ID NO[.]:2), X87368 (CPD; CYP90A) (SEQ ID. NO:19), U54770 (tomato; CYP85) (SEQ ID NO:20), D64003 (cyanobacteria; CYP120) (SEQ ID NO:21), U32579 (maize; CYP88) (SEQ ID NO:22), U68234 (zebrafish; CYP26) (SEQ ID NO:23), and M13785 (human; CYP3A3X) (SEQ ID NO:24). Dashes indicate gaps introduced to maximize alignment. Domains indicated in Figure 2B are highlighted in a box. Amino acid residues that are conserved >50% between the compared sequences are highlighted by a reverse font, and identical residues between DWF4 and CPD are boxed and italicized. Open triangles are placed under the 100% conserved residues (SEQ ID NO:25). Closed triangles locate functionally important amino acid residues, for example, threonine (T) at 369, which is thought to bind molecular oxygen, and cysteine (C) at 516, which links to a heme prosthetic group by a thiolate bond. X's indicate mutated resudes in *dwf4* alleles. Multiple sequence alignment was performed using PILEUP in the Genetics Computer Group package, and box shading was made possible by the ALSCRIPT package (Barton (1993) *Protein Eng.* 6:37-40).

Paragraph beginning at page 30, lines 22-29 has been amended as follows:

Regulatory regions can be isolated from the *dwf4* gene and used in recombinant constructs for modulating the expression of the *dwf4* gene or a heterologous gene *in vitro* and/or *in vivo*. As shown in Figure 10, the coding region of the *dwf4* gene (designated by the open ~~light grey~~ bars) begins at nucleotide position 1133. The region of the gene spanning nucleotide positions 990-1132 of Figure 10 includes the *dwf4* promoter. This region may be used in its entirety or fragments of the region may be isolated which provide the ability to direct expression of a coding sequence linked thereto.

In the claims:

Claims 5-10, 12, 14-17 and 19-45 have been cancelled.

Claims 58-94 have been added.